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<110> Takeda Chemical Industries, Ltd.

<120> Novel Polypeptide and its Use

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ATTTCTCTGG CTAGTGCTCA AGAAGATTAT AATGCCCCGG ACTGTAGATT CATTAACGTT 180

AAAAAAGGGC AGCAGATCTA TGTGTACTCA AAGCTGGTAA AAGAAAATGG AGCTGGAGAA 240

TTTTGGGCTG GCAGTGTTTA TGGTGATGGC CAGGACGAGA TGGGAGTCGT GGGTTATTTC 300

CCCAGGAACT TGGTCAAGGA ACAGCGTGTG TACCAGGAAG CTACCAAGGA AGTTCCCACC 360

ACGGATATTG ACTTCTTCTG CGAG 384

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Ala Val

18

<210> 6

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1 5 10 15

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20 25 30

Ala Asp Asp Glu Cys Val Tyr Thr Ile Ser Leu Ala Ser Ala Gln Glu
35 40 45

Asp Tyr Asn Ala Pro Asp Cys Arg Phe Ile Asn Val Lys Lys Gly Gln
50 55 60

Gln Ile Tyr Val Tyr Ser Lys Leu Val Lys Glu Asn Gly Ala Gly Glu
65 70 75 80
Phe Trp Ala Gly Ser Val Tyr Gly Asp Gly Gln Asp Glu Met Gly Val
85 90 95
Val Gly Tyr Phe Pro Arg Asn Leu Val Lys Glu Gln Arg Val Tyr Gln
100 105 110
Glu Ala Thr Lys Glu Val Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu
115 120 125 128

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ATTTCTCTGG CAAGAGCACA GGAAGATTAC AATGCCCCAG ACTGTAGGTT CATCGATGTC 180

AAGAAAGGGC AGCAGATCTA TGTTTACTCC AAGCTGGTAA CAGAAAACGG AGCTGGAGAG 240

TTTTGGGCTG GCAGTGTTTA TGGTGACCAC CAGGATGAGA TGGGAATTGT AGGTTATTTC 300

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Ala Gly
18

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Met Ala Arg Ile Leu Ile Leu Leu Leu Gly Gly Leu Val Val Leu Cys
1 5 10 15

Ala Gly His Gly Val Phe Met Asp Lys Leu Ser Ser Lys Lys Leu Cys
20 25 30

Ala Asp Glu Glu Cys Val Tyr Thr Ile Ser Leu Ala Arg Ala Gln Glu
35 40 45

Asp Tyr Asn Ala Pro Asp Cys Arg Phe Ile Asp Val Lys Lys Gly Gln
50 55 60

Gln Ile Tyr Val Tyr Ser Lys Leu Val Thr Glu Asn Gly Ala Gly Glu
65 70 75 80
Phe Trp Ala Gly Ser Val Tyr Gly Asp His Gln Asp Glu Met Gly Ile
85 90 95
Val Gly Tyr Phe Pro Ser Asn Leu Val Lys Glu Gln Arg Val Tyr Gln
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Glu Ala Thr Lys Glu Ile Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu
115 120 125 128

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ATCTCACCTT TAGCCCCTGG AATG 24

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AACGTTAAAA AAGGGCAGCA GATCTATGTG TACTCAAAGC TGGTAAAAGA AAATGGAGCT 180

GGAGAATTTT GGGCTGGCAG TGTTTATGGT GATGGCCAGG ACGAGATGGG AGTCGTGGGT 240

TATTTCCCCA GGAACTTGGT CAAGGAACAG CGTGTGTACC AGGAAGCTAC CAAGGAAGTT 300

CCCACCACGG ATATTGACTT CTTCTGCGAG 330

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His Gly Ile Phe Met Asp Arg Leu Ala Ser Lys Lys Leu Cys Ala Asp
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Asp Glu Cys Val Tyr Thr Ile Ser Leu Ala Ser Ala Gln Glu Asp Tyr
20 25 30

Asn Ala Pro Asp Cys Arg Phe Ile Asn Val Lys Lys Gly Gln Gln Ile
35 40 45

Tyr Val Tyr Ser Lys Leu Val Lys Glu Asn Gly Ala Gly Glu Phe Trp
50 55 60

Ala Gly Ser Val Tyr Gly Asp Gly Gln Asp Glu Met Gly Val Val Gly
65 70 75 80

Tyr Phe Pro Arg Asn Leu Val Lys Glu Gln Arg Val Tyr Gln Glu Ala
85 90 95

Thr Lys Glu Val Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu
100 105 110

<210> 25

<211> 330

<212> DNA

<213> Mouse

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GATGTCAAGA AAGGGCAGCA GATCTATGTT TACTCCAAGC TGGTAACAGA AAACGGAGCT 180
GGAGAGTTTT GGGCTGGCAG TGTTTATGGT GACCACCAGG ATGAGATGGG AATTGTAGGT 240
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Glu Glu Cys Val Tyr Thr Ile Ser Leu Ala Arg Ala Gln Glu Asp Tyr
20 25 30

Asn Ala Pro Asp Cys Arg Phe Ile Asp Val Lys Lys Gly Gln Gln Ile
35 40 45

Tyr Val Tyr Ser Lys Leu Val Thr Glu Asn Gly Ala Gly Glu Phe Trp
50 55 60

Ala Gly Ser Val Tyr Gly Asp His Gln Asp Glu Met Gly Ile Val Gly
65 70 75 80

Tyr Phe Pro Ser Asn Leu Val Lys Glu Gln Arg Val Tyr Gln Glu Ala

85 90 95

Thr Lys Glu Ile Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu

100 105 110

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AAGCTCTGTG CAGATGATGA GTGTGTCTAT ACTATTTCTC TGGCTAGTGC TCAAGAAGAT 180

TATAATGCCC CGGACTGTAG ATTCATTAAC GTTAAAAAAG GGCAGCAGAT CTATGTGTAC 240

TCAAAGCTGG TAAAAGAAAA TGGAGCTGGA GAATTTTGGG CTGGCAGTGT TTATGGTGAT 300

GGCCAGGACG AGATGGGAGT CGTGGGTTAT TTCCCCAGGA ACTTGGTCAA GGAACAGCGT 360
GTGTACCAGG AAGCTACCAA GGAAGTTCCC ACCACGGATA TTGACTTCTT CTGCGAGTAA 420
TAAATTAGTT AAAACTGCAA ATAGAAAGAA AACACCAAAA ATAAAGAAAA GAGCAAAAGT 480
GGCCAAAAAA TGCATGTCTG TAATTTTGGA CTGACGTTTT AAGAATTTGT TACCTTACAG 540
AAGAGCAAGG GCTTAGGGGT TGGAGGTGGC AGATAAAAGA GGATTTTCAA CTCAAATCTT 600
GTTTCCTGCT GGCCTGGTCT GCCCACGAGC TAGAGCGGGG AAATGTTGAG CTCAAATGGG 660
TAAATTGAGA CCAGAAAATT ATTTTTTCAA CCTAGAGAAT CTCCTCTTAC AGGGGGATGC 720
ATATAACAGA TCATGTATGT GTAGTTATTT CTAAGTAGTA ATTCTTCCCA GCTCTTTGAT 780
TTGCCATATA TAAAATAGGT GGGTCGTATG TCTTCCCTTT AGACATGATG TTTTCTACTC 840
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TGTCTATACT ATTTCTCTGG CAAGAGCACA GGAAGATTAC AATGCCCCAG ACTGTAGGTT 180
CATCGATGTC AAGAAAGGGC AGCAGATCTA TGTTTACTCC AAGCTGGTAA CAGAAAACGG 240
AGCTGGAGAG TTTTGGGCTG GCAGTGTTTA TGGTGACCAC CAGGATGAGA TGGGAATTGT 300
AGGTTATTTC CCCAGCAACT TGGTGAAGGA GCAGCGTGTA TACCAGGAGG CCACCAAGGA 360
GATCCCAACC ACGGATATTG ACTTCTTCTG TGAATAAGAA ATTAATTAAA ACAGCAGATA 420
AAACAGAAAC ACCAGTGATG AAGAAGAGAA GAAGTGGAAA TAACTGAACC TGTGTATCCG 480
TACCTTCCTG GCTTTATTTG GTGGCAGGAG GTTGGAGCTT GAAGGTGCTA AGATATGGAA 540
ATTGTCAACT CAGTCTTGTT TACTCTTGCC CCGGTCTTTC CACCAACTGC GACTAAGTGC 600
TGTGTGAATC ATATAGGTCA TTTATAACCC AATACTTAGC TTTCAGCGAG GAGAATCTTT 660
ATTTACTCAG TGATGAACAT ATAAGGTGTT TTATCTGTAG TTATTTCTAA ATGGTCATTC 720
TCCCCAGCTC TGACTCCATG TCCTTAAGCT TGCTGAGTTA GAAGTCTGAC TTTTGGGTGT 780

GTTTTCTGTT ATTTGTCTCT CTGGTCATGT GAAGTCTTAA TAATGTATTT GTCATGATAA 840

CTTCCTATTG TTACTTTTTA TATCTGATGC CCTTGGATAG AAGAATGTTA GGTATAAAAC 900

AAGTTTTTGT ACTCCCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA 947

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Thr Asp Ile Asp Cys
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<211> 41

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<211> 87

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<400> 39

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Thr Ile Ser Leu Ala Arg Ala Gln Glu Asp Tyr Asn Ala Pro Asp Cys
20 25 30

Arg Phe Ile Asn Val Lys Lys Gly Gln Gln Ile Tyr Val Tyr Ser Lys
35 40 45

Leu Val Thr Glu Asn Gly Ala Gly Ala Phe Trp Ala Gly Ser Val Tyr
50 55 60

Gly Asp His Gln Asp Glu Met Gly Ile Val Gly Tyr Phe Pro Ser Asn
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Leu Val Arg Glu Gln Arg Val
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<211> 261

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<213> Rat

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GCAGCAGATC TATGTTTATT CCAAGCTGGT AACAGAAAAT GGAGCTGGGG CATTCTGGGC 180

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<211> 307

<212> DNA

<213> Rat

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TTCATCAATG TCAAGAAAGG GCAGCAGATC TATGTTTATT CCAAGCTGGT AACAGAAAAT 180

GGAGCTGGGG CATTCTGGGC TGGCAGTGTT TATGGTGACC ACCAGGATGA GATGGGAATT 240

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<211> 29

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<210> 46

<211> 384

<212> DNA

<213> Rat

<400> 46

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ATTTCTCTGG CAAGAGCACA GGAAGACTAC AATGCCCCGG ACTGTAGGTT CATCAATGTC 180
AAGAAAGGGC AGCAGATCTA TGTTTATTCC AAGCTGGTAA CAGAAAATGG AGCTGGGGCA 240
TTCTGGGCTG GCAGTGTTTA TGGTGACCAC CAGGATGAGA TGGGAATTGT GGGTTATTTC 300
CCCAGCAACT TGGTTAGAGA GCAACGAGTG TACCAGGAGG CCACCAAGGA GATTCCAACC 360
ACGGATATTG ACTTCTTCTG TGAA 384

<210> 47
<211> 128
<212> PRT
<213> Rat
<400> 47

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Ala Gly His Gly Met Phe Met Asp Lys Leu Ser Ser Lys Lys Leu Cys
20 25 30
Ala Asp Glu Glu Cys Val Tyr Thr Ile Ser Leu Ala Arg Ala Gln Glu
35 40 45
Asp Tyr Asn Ala Pro Asp Cys Arg Phe Ile Asn Val Lys Lys Gly Gln
50 55 60
Gln Ile Tyr Val Tyr Ser Lys Leu Val Thr Glu Asn Gly Ala Gly Ala
65 70 75 80
Phe Trp Ala Gly Ser Val Tyr Gly Asp His Gln Asp Glu Met Gly Ile
85 90 95
Val Gly Tyr Phe Pro Ser Asn Leu Val Arg Glu Gln Arg Val Tyr Gln
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Glu Ala Thr Lys Glu Ile Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu
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<211> 330
<212> DNA

<213> Rat

<400> 48

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GGGGCATTCT GGGCTGGCAG TGTTTATGGT GACCACCAGG ATGAGATGGG AATTGTGGGT 240

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CCAACCACGG ATATTGACTT CTTCTGTGAA 330

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<400> 49

His Gly Met Phe Met Asp Lys Leu Ser Ser Lys Lys Leu Cys Ala Asp
5 10 15

Glu Glu Cys Val Tyr Thr Ile Ser Leu Ala Arg Ala Gln Glu Asp Tyr
20 25 30

Asn Ala Pro Asp Cys Arg Phe Ile Asn Val Lys Lys Gly Gln Gln Ile
35 40 45

Tyr Val Tyr Ser Lys Leu Val Thr Glu Asn Gly Ala Gly Ala Phe Trp
50 55 60

Ala Gly Ser Val Tyr Gly Asp His Gln Asp Glu Met Gly Ile Val Gly
65 70 75 80

Tyr Phe Pro Ser Asn Leu Val Arg Glu Gln Arg Val Tyr Gln Glu Ala
85 90 95

Thr Lys Glu Ile Pro Thr Thr Asp Ile Asp Phe Phe Cys Glu
100 105 110

<210> 50

<211> 18

<212> PRT

<213> Rat

<400> 50

Met Ala Arg Ile Leu Ile Leu Leu Leu Gly Gly Leu Val Ala Leu Cys
5 10 15

Ala Gly

18